



Blast 2 Sequences results

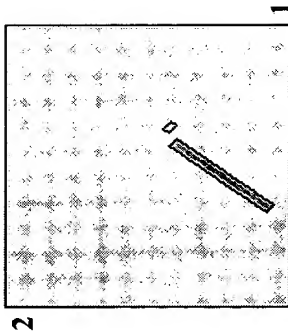
PubMed Entrez BLAST OMIM Taxonomy Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.10 [Oct-19-2004]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ Align

Sequence 1 lc|seq_1 Length 8509 (1 .. 8509)

Sequence 2 lc|seq_2 Length 5859 (1 .. 5859)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence

Score = 3857 bits (2006), Expect = 0.0
Identities = 2006/2006 (100%)
Strand = Plus / Plus



Query: 2955 ggcaatgggtcgaaattcatagaaattttgtgtgaggtgcgtagcggctctgacaggggtg 3014
|||||
Sbjct: 402 ggcaatgggtcgaaattcatagaaattttgtgtgaggtgcgtagcggctctgacaggggtg 461

Query: 3015 ctgcgaggagatctctgtgtctcaggtagggcgacaaatggagaggtgttagttgccccctg 3074



|||||
Sbjct: 462 ctgcgcggagatctctggtctcaggtaggcgacaatggagagggttagttgccccctg 521

Query: 3075 tatcgctctctgcgtggcgcattgggtcatcctgcccgacatatgatatccgctagag 3134
|||||
Sbjct: 522 tatcgctctctgcgtggcgcattgggtcatcctgcccgacatatgatatccgctagag 581

Query: 3135 gattactgatatgtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 3194
|||||
Sbjct: 582 gattactgatatgtttctgcctgtcgggcttgcgggcttgcgggcttgcgggcttgtc 641

Query: 3195 gggcctgtccctcttctgtcccgccctgtccctcactttttcacaaatcaaaaaatgggcgaagc 3254
|||||
Sbjct: 642 gggcctgtccctcttctgtcccgccctgtccctcactttttcacaaatcaaaaaatgggcgaagc 701

Query: 3255 ccttcttgttctatagttcttctatagttcctacgaaaaattacacataattatcaatagctt 3314
|||||
Sbjct: 702 ccttcttgttctatagttcttctatagttcctacgaaaaattacacataattatcaatagctt 761

Query: 3315 attcgcttaaaaggaggagtaattggccgcgcaaaaggagtaattggccgcgcaaaaggaggt 3374
|||||
Sbjct: 762 attcgcttaaaaggaggagtaattggccgcgcaaaaggagtaattggccgcgcaaaaggaggt 821

Query: 3375 aattggccgcgcaaaaggaggagtaattggccgcgatatcgggtgtttacatggggagggaatcc 3434
|||||
Sbjct: 822 aattggccgcgcaaaaggaggagtaattggccgcgatatcgggtgtttacatggggagggaatcc 881

Query: 3435 ccttaatactttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 3494
|||||
Sbjct: 882 ccttaatactttctcccccatgggaaagacacacaaagtggccgcagaccgggccttcgac 941

Query: 3495 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatcgccaatccgccc 3554
|||||
Sbjct: 942 cagacaaaaaactgtgctccctgcgcgaggtggcgagaggggtctatatcgccaatccgccc 1001

Query: 3555 cgcctgcaggcgctcaagctcatgcatttaatatagccactgcggcgccgcatggct 3614
|||||
Sbjct: 1002 cgcctgcaggcgctcaagctcatgcatttaatatagccactgcggcgccgcatggct 1061

Query: 3615 gatgatgtgcgcccatgaaatcgggctgcccagacattcgcgcaatcgacggcatgaaaaac 3674
|||||
Sbjct: 1062 gatgatgtgcgcccatgaaatcgggctgcccagacattcgcgcaatcgacggcatgaaaaac 1121

Query: 3675 catgaccgtgagagcctgacccccgctgttcgaggagctagccgctgcgggtgttgacccat 3734
|||||
Sbjct: 1122 catgaccgtgagagcctgacccccgctgttcgaggagctagccgctgcgggtgttgacccat 1181

Query: 3735 gatgaccctgcaaaagatgatcgtgacagtcggcggttggtcgcgatgaggcgcaatagac 3794
|||||
Sbjct: 1182 gatgaccctgcaaaagatgatcgtgacagtcggcggttggtcgcgatgaggcgcaatagac 1241

Query: 3795 taccgccaggaggcaagcgcggaactcctagtgcgtggaccttcgggagtagacattccgt 3854
|||||
Sbjct: 1242 taccgccaggaggcaagcgcggaactcctagtgcgtggaccttcgggagtagacattccgt 1301

Query: 3855 cgtatggcggcgagtcgaaccactgggccattctcgaccgtcaaaacgggtattccatctc 3914
|||||
Sbjct: 1302 cgtatggcggcgagtcgaaccactgggccattctcgaccgtcaaaacgggtattccatctc 1361

Query: 3915 ggtagtaagtattccgtgctgctgttcagcacgctctctagtctcgccaatcttgatcgg 3974
|||||
Sbjct: 1362 ggtagtaagtattccgtgctgctgttcagcacgctctctagtctcgccaatcttgatcgg 1421

Query: 3975 atgagcgcgaaaaacctttacgggtccccgagttgcggcgctccttgagtgccccgagggg 4034
|||||
Sbjct: 1422 atgagcgcgaaaaacctttacgggtccccgagttgcggcgctccttgagtgccccgagggg 1481

Query: 4035 aagatggttcgcttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 4094
|||||
Sbjct: 1482 aagatggttcgcttggaacgacgcttaacagatttgctctcaaacctgcactggatgagatc 1541

Query: 4095 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 4154
|||||
Sbjct: 1542 aaccatttatcgcgtctgacattgacggcaaaagccgaccaagattggccgtagcgtggca 1601

Query: 4155 agtgtactataggctgggaagtgaagacgacccaacccgtgccaggcgagctggcg 4214
|||||
Sbjct: 1602 agtgtactataggctgggaagtgaagacgacccaacccgtgccaggcgagctggcg 1661

Query: 4215 ggttccaaggctcgcgagatgctcgtcgcagaggggcagcggaacgatatgccccctcc 4274
|||||
Sbjct: 1662 ggttccaaggctcgcgagatgctcgtcgcagaggggcagcggaacgatatgccccctcc 1721

Query: 4275 ttcccagaagcggcggtcgcagatcacctacagtccacgttggtggagctgaaacgctctgct 4334
|||||
Sbjct: 1722 ttcccagaagcggcggtcgcagatcacctacagtccacgttggtggagctgaaacgctctgct 1781

Query: 4335 ggcagcaacaaggacaaacgatctgatcgccctcagactccggcggtttctgtcgggagaga 4394
|||||
Sbjct: 1782 ggcagcaacaaggacaaacgatctgatcgccctcagactccggcggtttctgtcgggagaga 1841

Query: 4395 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagatttctgcgcaaaagta 4454
|||||
Sbjct: 1842 ggcgtgcgtctggacgctgcaaaacatcgaaaaaactgttttagatttctgcgcaaaagta 1901

Query: 4455 gggaaggtttgagttttgaggtatttcaccgcaatagtggttaaatgactttcgtgaaaacg 4514
|||||
Sbjct: 1902 gggaaggtttgagttttgaggtatttcaccgcaatagtggttaaatgactttcgtgaaaacg 1961

Query: 4515 atgtgcaatatagcggtaagactatgaaatcacacggctggacaggctgcacaaagcaacgg 4574
|||||
Sbjct: 1962 atgtgcaatatagcggtaagactatgaaatcacacggctggacaggctgcacaaagcaacgg 2021

Query: 4575 gtgtggcgaccgcaaccatcactcggcggtataaaagcggtataatttccgggtaaaaaag 4634
|||||
Sbjct: 2022 gtgtggcgaccgcaaccatcactcggcggtataaaagcggtataatttccgggtaaaaaag 2081

Query: 4635 atgaatctggggcatgggttatagatcctgcagaattgcacagagtggttctctccattt 4694
|||||
Sbjct: 2082 atgaatctggggcatgggttatagatcctgcagaattgcacagagtggttctctccattt 2141

Query: 4695 caaagaaatacacaccgaaacacacctaacaacgcaagtatatgttaagcgtgatgaaacacatg 4754
|||||
Sbjct: 2142 caaagaaatacacaccgaaacacacctaacaacgcaagtatatgttaagcgtgatgaaacacatg 2201

Query: 4755 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgcctttat 4814
|||||
Sbjct: 2202 aaatgacctcagaaaaatcagcgcattagagcgtgaagttcggactttacgcgatgcctttat 2261

Query: 4815 ctgatgccaggaggatcgcgacaaaatggcgcacatggccgagcgtctttcaatttcat 4874
|||||
Sbjct: 2262 ctgatgccaggaggatcgcgacaaaatggcgcacatggccgagcgtctttcaatttcat 2321

Query: 4875 caccgatgagagaggaagaccgccccctcaaaaaaagatggtggaagatatcttgat 4934
|||||
Sbjct: 2322 caccgatgagagaggaagaccgccccctcaaaaaaagatggtggaagatatcttgat 2381

Query: 4935 cctgggcttcaggagccttgccttta 4960
|||||
Sbjct: 2382 cctgggcttcaggagccttgccttta 2407

Score = 208 bits (108), Expect = 2e-49
Identities = 108/108 (100%)
Strand = Plus / Plus



Query: 5364 tactggcgaaaaaacgcgatattgaggaagccagatggccgcacttttagaggcggaagcctata 5423
|||||
Sbjct: 2406 tactggcgaaaaaacgcgatattgaggaagccagatggccgcacttttagaggcggaagcctata 2465

Query: 5424 acgagtaccaaaaacactagaagccagattgaggaataatagggaaacgtg 5471

Blast Result

|||||
Sbjct: 2466 acgagtacaaacactagaaagccagattgaggaaaaatagggaacgtg 2513

CPU time: 0.06 user secs. 0.02 sys. secs 0.08 total secs.

Lambda K H
1.33 0.621 1.12

Gapped
Lambda K H
1.33 0.621 1.12

Matrix: blastn matrix:1 -2
Gap Penalties: Existence: 5, Extension: 2
Number of Sequences: 1
Number of Hits to DB: 1061
Number of extensions: 43
Number of successful extensions: 14
Number of sequences better than 10.0: 1
Number of HSP's better than 10.0 without gapping: 1
Number of HSP's gapped: 2
Number of HSP's successfully gapped: 2
Number of extra gapped extensions for HSPs above 10.0: 0
Length of query: 8509
Length of database: 12,527,565,053
Length adjustment: 28
Effective length of query: 8481
Effective length of database: 12,527,565,025
Effective search space: 106246278977025
Effective search space used: 106246278977025
Neighboring words threshold: 0
Window for multiple hits: 0
X1: 11 (21.1 bits)
X2: 26 (50.0 bits)
X3: 26 (50.0 bits)
S1: 12 (23.8 bits)
S2: 23 (44.9 bits)